

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/536,716  
Source: 1 FWP  
Date Processed by STIC: 6/14/06

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IFWP

## RAW SEQUENCE LISTING

DATE: 06/14/2006

PATENT APPLICATION: US/10/536,716

TIME: 10:36:15

Input Set : E:\8932003W.APP

Output Set: N:\CRF4\06142006\J536716.raw

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3 <110> APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA
5 <120> TITLE OF INVENTION: HOMOLOGOUS RECOMBINATION IN MULTIPOTENT ADULT
6   PROGENITOR CELLS
8 <130> FILE REFERENCE: 890003-2003.WO
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/536,716
C--> 11 <141> CURRENT FILING DATE: 2005-05-25
13 <150> PRIOR APPLICATION NUMBER: 60/429,631
14 <151> PRIOR FILING DATE: 2002-11-27
16 <150> PRIOR APPLICATION NUMBER: PCT/US02/04652
17 <151> PRIOR FILING DATE: 2002-02-14
19 <150> PRIOR APPLICATION NUMBER: PCT/US00/21387
20 <151> PRIOR FILING DATE: 2000-08-04
22 <160> NUMBER OF SEQ ID NOS: 5
24 <170> SOFTWARE: PatentIn Ver. 3.2
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1674
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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34 ttccaggagt tccaaaggaa gatgtatgaa gccttgaaag agatggattc taatacagtc 180
35 attgaaagat tccccacaat tgggtcaactg ttggcaaaag cttggttgaa tccttttatt 240
36 ttagcatatg atgaaagcca aaaaattcta atatggtgct tatgttgtct aattaacaaa 300
37 gaaccacaga attctggaca atcaaaactt aactcctgga tacagggtgt attatctcat 360
38 atactttcag cactcagatt tgataaagaa gttgctcttt tcaactcaagg tcttgggtat 420
39 gcacctatag attactatcc tggtttgctt aaaaatatgg ttttatcatt agcgtctgaa 480
40 ctccagagaga atcatcttaa tggatttaac actcaaaggc gaatggctcc cgagcgagt 540
41 gcgtccctgt cagcagtttg tgtcccactt attacccctga cagatgttga cccctggtg 600
42 gaggtctctc tcatctgtca tggacgtgaa cctcaggaaa tccctccagcc agagttcttt 660
43 gaggtctgta acgaggccat tttgctgaag aagattttct tccccatgtc agctgtagtc 720
44 tgctcttggt ttccggcacct tcccagcctt gaaaaagcaa tgctgcatct ttttgaaaag 780
45 ctaatctcca gtgagagaaa ttgtctgaga aggatcgaa gctttataaa agattcatcg 840
46 ctgctcaag cagcctgcca cctgccata ttccgggttg ttgatgagat gttcagggtg 900
47 gcaactctgg aaaccgatgg ggccctggaa atcatagcca ctattcaggt gtttacgcag 960
48 tgctttgtag aagctctgga gaaagcaagc aagcagctgc ggtttgact caagacctac 1020
49 tttccttaca cttctccatc tcttgccatg gtgctgctgc aagaccctca agatatccct 1080
50 cggggacact ggctccagac actgaagcat atttctgaac tgctcagaga agcagttgaa 1140
51 gaccagactc atgggtcctg cggaggctcc tttgagagct ggttcctgtt cattcacttc 1200
52 ggaggatggg ctgagatggg ggcagagcaa ttactgatgt cggcagccga accccccacg 1260
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56 cctgcacaac agctgatcag gcaccttctc ctcaacttcc tgctctgggc tcctggaggc 1500  
 57 cacacgatcg cctgggatgt catcaccttg atggctcaca ctgctgagat aactcacgag 1560  
 58 atcattggct ttcttgacca gaccttgtag agatgggaatc gtcttgccat tgaaagccct 1620  
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62 &lt;210&gt; SEQ ID NO: 2

63 &lt;211&gt; LENGTH: 557

64 &lt;212&gt; TYPE: PRT

65 &lt;213&gt; ORGANISM: Homo sapiens

67 &lt;400&gt; SEQUENCE: 2

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 69 1 5 10 15  
 71 Gln Lys Leu Ser Val Trp Asp Gln Ala Ser Thr Leu Glu Thr Gln Gln  
 72 20 25 30  
 74 Asp Thr Cys Leu His Val Ala Gln Phe Gln Glu Phe Leu Arg Lys Met  
 75 35 40 45  
 77 Tyr Glu Ala Leu Lys Glu Met Asp Ser Asn Thr Val Ile Glu Arg Phe  
 78 50 55 60  
 80 Pro Thr Ile Gly Gln Leu Ala Lys Ala Cys Trp Asn Pro Phe Ile  
 81 65 70 75 80  
 83 Leu Ala Tyr Asp Glu Ser Gln Lys Ile Leu Ile Trp Cys Leu Cys Cys  
 84 85 90 95  
 86 Leu Ile Asn Lys Glu Pro Gln Asn Ser Gly Gln Ser Lys Leu Asn Ser  
 87 100 105 110  
 89 Trp Ile Gln Gly Val Leu Ser His Ile Leu Ser Ala Leu Arg Phe Asp  
 90 115 120 125  
 92 Lys Glu Val Ala Leu Phe Thr Gln Gly Leu Gly Tyr Ala Pro Ile Asp  
 93 130 135 140  
 95 Tyr Tyr Pro Gly Leu Leu Lys Asn Met Val Leu Ser Leu Ala Ser Glu  
 96 145 150 155 160  
 98 Leu Arg Glu Asn His Leu Asn Gly Phe Asn Thr Gln Arg Arg Met Ala  
 99 165 170 175  
 101 Pro Glu Arg Val Ala Ser Leu Ser Arg Val Cys Val Pro Leu Ile Thr  
 102 180 185 190  
 104 Leu Thr Asp Val Asp Pro Leu Val Glu Ala Leu Leu Ile Cys His Gly  
 105 195 200 205  
 107 Arg Glu Pro Gln Glu Ile Leu Gln Pro Glu Phe Phe Glu Ala Val Asn  
 108 210 215 220  
 110 Glu Ala Ile Leu Leu Lys Lys Ile Ser Leu Pro Met Ser Ala Val Val  
 111 225 230 235 240  
 113 Cys Leu Trp Leu Arg His Leu Pro Ser Leu Glu Lys Ala Met Leu His  
 114 245 250 255  
 116 Leu Phe Glu Lys Leu Ile Ser Ser Glu Arg Asn Cys Leu Arg Arg Ile  
 117 260 265 270  
 119 Glu Cys Phe Ile Lys Asp Ser Ser Leu Pro Gln Ala Ala Cys His Pro  
 120 275 280 285  
 122 Ala Ile Phe Arg Val Val Asp Glu Met Phe Arg Cys Ala Leu Leu Glu  
 123 290 295 300  
 125 Thr Asp Gly Ala Leu Glu Ile Ile Ala Thr Ile Gln Val Phe Thr Gln  
 126 305 310 315 320

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128 Cys Phe Val Glu Ala Leu Glu Lys Ala Ser Lys Gln Leu Arg Phe Ala
129           325           330           335
131 Leu Lys Thr Tyr Phe Pro Tyr Thr Ser Pro Ser Leu Ala Met Val Leu
132           340           345           350
134 Leu Gln Asp Pro Gln Asp Ile Pro Arg Gly His Trp Leu Gln Thr Leu
135           355           360           365
137 Lys His Ile Ser Glu Leu Leu Arg Glu Ala Val Glu Asp Gln Thr His
138           370           375           380
140 Gly Ser Cys Gly Gly Pro Phe Glu Ser Trp Phe Leu Phe Ile His Phe
141 385           390           395           400
143 Gly Gly Trp Ala Glu Met Val Ala Glu Gln Leu Leu Met Ser Ala Ala
144           405           410           415
146 Glu Pro Pro Thr Ala Leu Leu Trp Leu Leu Ala Phe Tyr Tyr Gly Pro
147           420           425           430
149 Arg Asp Gly Arg Gln Arg Ala Gln Thr Met Val Gln Val Lys Ala Val
150           435           440           445
152 Leu Gly His Leu Leu Ala Met Ser Arg Ser Ser Ser Leu Ser Ala Gln
153           450           455           460
155 Asp Leu Gln Thr Val Ala Gly Gln Gly Thr Asp Thr Asp Leu Arg Ala
156 465           470           475           480
158 Pro Ala Gln Gln Leu Ile Arg His Leu Leu Leu Asn Phe Leu Leu Trp
159           485           490           495
161 Ala Pro Gly Gly His Thr Ile Ala Trp Asp Val Ile Thr Leu Met Ala
162           500           505           510
164 His Thr Ala Glu Ile Thr His Glu Ile Ile Gly Phe Leu Asp Gln Thr
165           515           520           525
167 Leu Tyr Arg Trp Asn Arg Leu Gly Ile Glu Ser Pro Arg Ser Glu Lys
168           530           535           540
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171 545           550           555
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 21
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
181     primer
183 <400> SEQUENCE: 3
184 ctgccaacct gccatcttca g                                21
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188 <211> LENGTH: 21
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
194     primer
196 <400> SEQUENCE: 4
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Input Set : E:\8932003W.APP

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201 &lt;211&gt; LENGTH: 20

202 &lt;212&gt; TYPE: DNA

203 &lt;213&gt; ORGANISM: Artificial Sequence

205 &lt;220&gt; FEATURE:

206 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

207 primer

209 &lt;400&gt; SEQUENCE: 5

210 aggaaagtag gtcctgaggg

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**VERIFICATION SUMMARY**

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Input Set : E:\8932003W.APP

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date